

SEQUENCE LISTING

<110> Novartis Forschungsstiftung, Zweigniederlassung Friedrich Miescher
Institute for Biomedical Research

<120> Gene for increased somatic recombination

<130> 1-32546B

<160> 30

<170> PatentIn version 3.1

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 Arg Ile Gly Ala His Ser His Ile Arg Gly Leu Gly Leu Asp Ser Ala
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 ctc gag ccg cga gct gtt tcc gaa ggt atg gtc ggt caa gtg aag gcg 144
 Leu Glu Pro Arg Ala Val Ser Glu Gly Met Val Gly Gln Val Lys Ala
 35 40 45
 cgt aaa gcc gcc ggt gta atc ctt cag atg att aga gaa ggg aaa atc 192
 Arg Lys Ala Ala Gly Val Ile Leu Gln Met Ile Arg Glu Gly Lys Ile
 50 55 60
 gcg ggt cgg gct att cta ata gcg ggt caa ccc gga acg ggt aag aca 240
 Ala Gly Arg Ala Ile Leu Ile Ala Gly Gln Pro Gly Thr Gly Lys Thr
 65 70 75 80
 gcg att gca atg ggt atg gcg aaa tct ctt ggc ttg gaa act cct ttt 288
 Ala Ile Ala Met Gly Met Ala Lys Ser Leu Gly Leu Glu Thr Pro Phe
 85 90 95
 gcg atg att gca gga agt gaa att ttc tca tta gag atg tca aag aca 336
 Ala Met Ile Ala Gly Ser Glu Ile Phe Ser Leu Glu Met Ser Lys Thr
 100 105 110
 gaa gct ttg act cag tct ttt cgt aaa gcg att ggt gtt agg atc aaa 384
 Glu Ala Leu Thr Gln Ser Phe Arg Lys Ala Ile Gly Val Arg Ile Lys
 115 120 125
 gaa gag aca gag gtt att gaa gga gaa gtt gtt gag gtt cag att gat 432
 Glu Glu Thr Glu Val Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp
 130 135 140

agg Arg 145	cct Pro	gct Ala	tct Ser	tct Ser	ggg Gly 150	gtt Val	gct Ala	tcc Ser	aag Lys	tca Ser 155	ggg Gly	aag Lys	atg Met	act Thr	atg Met 160	480
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gag Glu	gct Ala	ttg Leu	aac Asn 180	aag Lys	gag Glu	aaa Lys	gtg Val	cag Gln 185	agt Ser	ggg Gly	gat Asp	gtt Val	att Ile 190	gcc Ala	att Ile	576
gat Asp	aaa Lys	gct Ala 195	act Thr	ggg Gly	aag Lys	att Ile	act Thr 200	aag Lys	ctt Leu	gga Gly	aga Arg	tcg Ser 205	ttt Phe	tcg Ser	agg Arg	624
tct Ser	cgt Arg 210	gat Asp	tat Tyr	gat Asp	gct Ala	atg Met 215	ggg Gly	gcg Ala	cag Gln	acc Thr	aag Lys 220	ttt Phe	gtg Val	cag Gln	tgc Cys	672
cct Pro 225	gaa Glu	ggg Gly	gag Glu	ttg Leu	cag Gln 230	aag Lys	agg Arg	aaa Lys	gag Glu	gtt Val 235	gta Val	cat His	tgt Cys	gtc Val	act Thr 240	720
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cag Gln 385	ctt Leu	ttg Leu	aca Thr	ttg Leu	atc Ile 390	gga Gly	cgt Arg	gat Asp	aca Thr	tct Ser 395	cta Leu	agg Arg	tat Tyr	gcg Ala	att Ile 400	1200
cat His	ctt Leu	ata Ile	acc Thr	gca Ala	gct Ala	gca Ala	ttg Leu	tca Ser	tgc Cys	cag Gln	aaa Lys	cgg Arg	aaa Lys	ggg Gly	aaa Lys	1248

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Val	Arg	Arg	Ser	Met	Gln	Tyr	Leu	Val	Glu	Tyr	Gln	Ser	Gln	Tyr	Met	
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Phe	Ser	Glu	Pro	Ile	Lys	Asn	Asp	Glu	Ala	Ala	Ala	Glu	Asp	Glu	Gln	
	450					455					460					
gat	gct	atg	cag	atc	tga	ggatccacct	ctgtttgcct	tatttatcat								1440
Asp	Ala	Met	Gln	Ile												
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<213> Arabidopsis thaliana

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			100					105					110		

Glu	Ala	Leu	Thr	Gln	Ser	Phe	Arg	Lys	Ala	Ile	Gly	Val	Arg	Ile	Lys
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Glu Ile Arg Cys Gln Glu Glu Asp Val Glu Met Asn Glu Glu Ala Lys
370 375 380

Gln Leu Leu Thr Leu Ile Gly Arg Asp Thr Ser Leu Arg Tyr Ala Ile
385 390 395 400

His Leu Ile Thr Ala Ala Ala Leu Ser Cys Gln Lys Arg Lys Gly Lys
405 410 415

Val Val Glu Val Glu Asp Ile Gln Arg Val Tyr Arg Leu Phe Leu Asp
420 425 430

Val Arg Arg Ser Met Gln Tyr Leu Val Glu Tyr Gln Ser Gln Tyr Met
435 440 445

Phe Ser Glu Pro Ile Lys Asn Asp Glu Ala Ala Ala Glu Asp Glu Gln
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Ser His Ile Arg Gly Leu Gly Leu Asp Ser Val Leu Glu Pro Arg
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gcc gta tcc gaa gga atg gtt ggt caa atc aaa gca cgt aaa gcc gcc 156
Ala Val Ser Glu Gly Met Val Gly Gln Ile Lys Ala Arg Lys Ala Ala
20 25 30
gga gta acc ctc gag ttg atc aga gac ggc aaa atc tcg ggt cgg gct 204
Gly Val Thr Leu Glu Leu Ile Arg Asp Gly Lys Ile Ser Gly Arg Ala
35 40 45
ata ctt ata gcg ggt caa ccc gga acg ggt aaa atc gca ata gca atg 252
Ile Leu Ile Ala Gly Gln Pro Gly Thr Gly Lys Ile Ala Ile Ala Met
50 55 60
ggt ata gca aaa tca ctt gga caa gaa aca cca ttc act atg att gca 300
Gly Ile Ala Lys Ser Leu Gly Gln Glu Thr Pro Phe Thr Met Ile Ala

65	70	75	
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caa gct ttt cgt aaa gct att ggt gtt agg atc aaa gaa gag act gac Gln Ala Phe Arg Lys Ala Ile Gly Val Arg Ile Lys Glu Glu Thr Asp 100 105 110			396
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gag ctt gag aag agg aag gag gtt ttg cat tct gtc aca ctt cat gag Glu Leu Glu Lys Arg Lys Glu Val Leu His Ser Val Thr Leu His Glu 210 215 220			732
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gct aca aac aga gga atg aca aca atc cga gga aca aac cag ata tca Ala Thr Asn Arg Gly Met Thr Thr Ile Arg Gly Thr Asn Gln Ile Ser 305 310 315			1020
gca cat ggg atc cca atc gat ttt ctt gac cgt ctt ctt att atc aca Ala His Gly Ile Pro Ile Asp Phe Leu Asp Arg Leu Leu Ile Ile Thr 320 325 330 335			1068

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 Thr Gln Pro Tyr Thr Gln Asp Glu Ile Arg Asn Ile Leu Glu Ile Arg
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 Cys Gln Glu Glu Asp Val Glu Met Asn Glu Glu Ala Lys Gln Leu Leu
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 Asn Ala Ala Ala Leu Ala Cys Leu Lys Arg Lys Gly Lys Val Val Glu
 385 390 395
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 Ile Gln Asp Ile Glu Arg Val Tyr Arg Leu Phe Leu Asp Thr Lys Arg
 400 405 410 415
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 Ser Met Gln Tyr Leu Val Glu His Glu Ser Glu Tyr Leu Phe Ser Val
 420 425 430
 cct ata aaa aac aca cag gag gct act gca gga gaagaaacag aacacgaggc 1409
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<213> Arabidopsis thaliana

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 35 40 45

Leu Ile Ala Gly Gln Pro Gly Thr Gly Lys Ile Ala Ile Ala Met Gly
 50 55 60

Ile Ala Lys Ser Leu Gly Gln Glu Thr Pro Phe Thr Met Ile Ala Gly
 65 70 75 80

Ser Glu Ile Phe Ser Leu Glu Met Ser Lys Thr Glu Ala Leu Thr Gln
 85 90 95

Ala Phe Arg Lys Ala Ile Gly Val Arg Ile Lys Glu Glu Thr Asp Val
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 Ile Glu Gly Glu Val Val Thr Ile Ser Ile Asp Arg Pro Ala Ser Ser
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 Met Glu Ser Asn Phe Asp Leu Gly Trp Lys Leu Ile Glu Pro Leu Asp
 145 150 155 160
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 165 170 175
 Gly Lys Ile Thr Lys Leu Gly Arg Ser Phe Thr Arg Ser Arg Asp Phe
 180 185 190
 Asp Val Met Gly Ser Lys Thr Lys Phe Val Gln Cys Pro Glu Gly Glu
 195 200 205
 Leu Glu Lys Arg Lys Glu Val Leu His Ser Val Thr Leu His Glu Ile
 210 215 220
 Asp Val Ile Asn Ser Arg Thr Gln Gly Tyr Leu Ala Leu Phe Thr Gly
 225 230 235 240
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 245 250 255
 Val Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val
 260 265 270
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 290 295 300
 Thr Asn Arg Gly Met Thr Thr Ile Arg Gly Thr Asn Gln Ile Ser Ala
 305 310 315 320
 His Gly Ile Pro Ile Asp Phe Leu Asp Arg Leu Leu Ile Ile Thr Thr
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 Gln Glu Glu Asp Val Glu Met Asn Glu Glu Ala Lys Gln Leu Leu Thr

355 360 365
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 Ala Ala Ala Leu Ala Cys Leu Lys Arg Lys Gly Lys Val Val Glu Ile
 385 390 395 400
 Gln Asp Ile Glu Arg Val Tyr Arg Leu Phe Leu Asp Thr Lys Arg Ser
 405 410 415
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<223>

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20 25 30

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Cys Lys Lys Asp Gly Ile Val Leu Cys Pro Gly Phe Thr Thr Thr His
35 40 45

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Ser Ile Pro Phe Val Asp Gly Glu Pro Ile Tyr Lys Gly Ser Ser Arg
50 55 60

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act aac att ggt gga tat cat gtc act gat tat tta aag cag ctt ctg 240
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65 70 75 80

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Thr	Thr	Ala	Ala	Phe	Asp	Arg	Gly	Lys	Gly	Glu	Asp	Thr	Phe	Gly	Ser	
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tca	tct	aga	ctt	cag	gaa	att	gat	cca	aca	ttt	gtg	cag	aaa	gta	gaa	1296
Ser	Ser	Arg	Leu	Gln	Glu	Ile	Asp	Pro	Thr	Phe	Val	Gln	Lys	Val	Glu	
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gga	gaa	ttg	agt	cag	aca	tca	ggg	gag	gtg	cca	cgc	gta	cgc	cca	tta	1344
Gly	Glu	Leu	Ser	Gln	Thr	Ser	Gly	Glu	Val	Pro	Arg	Val	Arg	Pro	Leu	
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Leu	Asp	Glu	Met	Ala	Gly	Thr	Ser	Ile	Arg	Arg	Leu	Pro	His	Asp	Glu	
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Pro	Val	Leu	Asp	Ala	Trp	Arg	Gly	Ala	Ser	Ala	Phe	Ala	Ala	Asn	Leu	
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gaa	gat	tgg	ctt	aga	aat	tat	caa	att	cga	tac	aac	tat	ttg	tga		1773
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Thr Asn Ile Gly Gly Tyr His Val Thr Asp Tyr Leu Lys Gln Leu Leu
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Glu Ile Arg Leu Phe Gln Glu Gly Arg Lys Glu Ala Glu Glu Lys Thr
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Gln Arg Leu Arg Glu Met Ala Glu Ala Lys Arg Val Ser Lys Ile Asn
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 Thr Glu Glu Asp Tyr Lys Ile Val Ile Gly Ile Glu Arg Phe Arg Cys
 450 455 460
 Pro Glu Ile Leu Phe His Pro Asn Leu Ile Gly Ile Asp Gln Val Gly
 465 470 475 480
 Leu Asp Glu Met Ala Gly Thr Ser Ile Arg Arg Leu Pro His Asp Glu
 485 490 495

Lys Glu Leu Glu Glu Arg Leu Thr Ser Ser Ile Leu Met Thr Gly Gly
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 Cys Ser Leu Leu Pro Gly Met Asn Glu Arg Leu Glu Cys Gly Ile Arg
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 Met Ile Arg Pro Cys Gly Ser Pro Ile Asn Val Val Arg Ala Met Asp
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 Pro Val Leu Asp Ala Trp Arg Gly Ala Ser Ala Phe Ala Ala Asn Leu
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 Gly Lys Asp Leu Val Asn His Gln Arg Ala Ile Asp Val Pro Pro Leu
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tta ttg tct tct tca tcg tct ctt ggt gcg ttt gat cag cta ccg atg 144
 Leu Leu Ser Ser Ser Ser Ser Leu Gly Ala Phe Asp Gln Leu Pro Met
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gat att cta gtc cag ata ctg atg atg atg gag cca aaa gat gct gtg 192
 Asp Ile Leu Val Gln Ile Leu Met Met Met Glu Pro Lys Asp Ala Val
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 Lys Leu Gly Leu Thr Cys Lys Ala Trp Lys Cys Val Ala Ser Gly Asn
 65 70 75 80

cgt ctc tgg ata ttt tat ctc cag tgt tct caa gag cca tgg gac tcc 288

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att Ile	tct Ser	agt Ser 115	caa Gln	tca Ser	gga Gly	gag Glu	ttg Leu 120	tcg Ser	ttt Phe	atg Met	cac His	att Ile 125	tat Tyr	agt Ser	cag Gln	384
agg Arg	gca Ala 130	caa Gln	gtt Val	cct Pro	ggc Gly	tct Ser 135	atc Ile	att Ile	att Ile	gat Asp	ggc Gly 140	ggc Gly	tct Ser	gga Gly	tat Tyr	432
tgt Cys 145	aag Lys	ttt Phe	ggc Gly	tgg Trp	agc Ser 150	aag Lys	tat Tyr	gcg Ala	tct Ser	cct Pro 155	tct Ser	gga Gly	cgt Arg	tct Ser	gct Ala 160	480
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 35 40 45
 Asp Ile Leu Val Gln Ile Leu Met Met Met Glu Pro Lys Asp Ala Val
 50 55 60
 Lys Leu Gly Leu Thr Cys Lys Ala Trp Lys Cys Val Ala Ser Gly Asn
 65 70 75 80

Arg Leu Trp Ile Phe Tyr Leu Gln Cys Ser Gln Glu Pro Trp Asp Ser
85 90 95

Ile Phe Phe Ala Glu Thr Ser Leu Arg Ser Gly Tyr Pro Leu Arg Met
100 105 110

Ile Ser Ser Gln Ser Gly Glu Leu Ser Phe Met His Ile Tyr Ser Gln
115 120 125

Arg Ala Gln Val Pro Gly Ser Ile Ile Ile Asp Gly Gly Ser Gly Tyr
130 135 140

Cys Lys Phe Gly Trp Ser Lys Tyr Ala Ser Pro Ser Gly Arg Ser Ala
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Thr Phe Leu Glu Phe Gly Asn Ile Glu Ser Pro Ile Tyr Ala Arg Leu
165 170 175

Gln Gln Phe Phe Ala Thr Ile Phe Thr Arg Met Gln Val Lys Pro Ser
180 185 190

Met Gln Pro Ile Val Val Ser Leu Pro Leu Cys His Phe Asp Asp Thr
195 200 205

Glu Ser Ala Lys Ala Ser Arg Arg Gln Leu Lys Thr Ala Ile Phe Asn
210 215 220

Val Leu Phe Asp Met Asn Val Pro Ala Val Cys Ala Val Asn Gln Ala
225 230 235 240

Val Leu Ala Leu Tyr Ala Ala Arg Arg Thr Ser Gly Ile Val Val Asn
245 250 255

Ile Gly Phe Gln Val Ile Thr Ile Leu Pro Ile Leu His Gly Lys Val
260 265 270

Met Arg Gln Val Gly Val Glu Val Ile Gly Phe Gly Ala Leu Lys Leu
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Thr Gly Phe Leu Lys Glu Lys Met Gln Glu Asn Asn Ile Ser Phe Gln
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Ser Leu Tyr Thr Val Arg Thr Leu Lys Glu Lys Leu Cys Tyr Val Ala
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 gtg gtg ttt ccg cag aat cag cac gtt act aaa gca gat tat gac gag 1056
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 Asp Trp Asp Ala Met Glu Asp Leu Leu Arg Tyr Val Val Tyr Thr Gly
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 Leu Gly Trp Glu Glu Gly Asn Glu Gly Asn Ile Leu Phe Thr Asp Pro
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 His Gly Lys Ile Asp Ile Ala Pro Val Leu Glu Gly Ala Val Gln His
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Phe Ala Gln Glu Leu Gly Lys Thr Asn Pro Ser Met Asn Leu Ser Met
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Ser Asp Val Glu Lys Leu Lys Glu Gln Tyr Ala Asn Cys Ala Glu Asp
 195 200 205

Glu Ile Ala Tyr Lys Lys Thr Gln Asn Cys Glu Ile Glu Gln His Thr
 210 215 220

Leu Pro Asp Gly Gln Val Ile Ser Ile Gly Arg Glu Arg Tyr Ser Val
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Gly Glu Ala Leu Phe Gln Pro Ser Ile Leu Gly Leu Glu Glu His Gly
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Ile Val Glu Gln Leu Val Arg Ile Ile Ser Thr Val Ser Ser Glu Asn
 260 265 270

His Arg Gln Leu Leu Glu Asn Thr Val Leu Cys Gly Gly Thr Thr Ser
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Met Thr Gly Phe Glu Ser Arg Phe Gln Lys Glu Ala Asn Leu Cys Ser
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Asn Leu Gly Met Tyr Ser Ala Trp Val Gly Gly Ala Ile Leu Ala Lys
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Val Val Ile Asn Leu Gly Ser Ala Asn Val Arg Val Gly Leu Ala Met	
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Asp Glu Lys Pro Phe Asn Val Pro Asn Cys Ile Ala Arg Tyr Ile Thr	
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Ser Leu Leu Lys Ile Leu Phe Leu Asp Glu Ser Ser Ser Ser Gly Ser	
100 105 110	
gca tct cgc aag atg ggg agg atc gac gga tac aat caa gcg agt acg	384
Ala Ser Arg Lys Met Gly Arg Ile Asp Gly Tyr Asn Gln Ala Ser Thr	
115 120 125	
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Ile Lys Lys Asp Ser Val Phe Thr Trp Thr Asp Val Tyr Glu Asp Glu	
130 135 140	
aaa att tct ctt gcc tca cca gca gaa act tct cct gat aaa ggt gat	480
Lys Ile Ser Leu Ala Ser Pro Ala Glu Thr Ser Pro Asp Lys Gly Asp	
145 150 155 160	
gct agt gca tct gaa gct gtt cct gat gtt act gac tct aaa gat act	528
Ala Ser Ala Ser Glu Ala Val Pro Asp Val Thr Asp Ser Lys Asp Thr	
165 170 175	
agt gag agt aaa cgc aag tat agg aaa atg att ttt ggt gaa gaa gct	576
Ser Glu Ser Lys Arg Lys Tyr Arg Lys Met Ile Phe Gly Glu Glu Ala	
180 185 190	
ttg aaa ata tcg cca aaa gag cca tat tgt tta tac cat cct att cgg	624
Leu Lys Ile Ser Pro Lys Glu Pro Tyr Cys Leu Tyr His Pro Ile Arg	
195 200 205	
aga ggt cac ttc aat gtt tcg cca cat tat tca gcg caa cgg gtt tgt	672
Arg Gly His Phe Asn Val Ser Pro His Tyr Ser Ala Gln Arg Val Cys	
210 215 220	
gag gac tta act gct atc ttg gac tgg att tta tta gag aaa ctt cat	720

Glu 225	Asp	Leu	Thr	Ala	Ile 230	Leu	Asp	Trp	Ile	Leu 235	Leu	Glu	Lys	Leu	His 240	
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gga Gly	gag Glu	cta Leu 275	tac Tyr	ttt Phe	aac Asn	tca Ser	gca Ala 280	gtt Val	gtc Val	cac His	caa Gln	gaa Glu 285	ggt Gly	cta Leu	tcg Ser	864
gcc Ala	gtt Val 290	ttt Phe	ggg Gly	aat Asn	ggt Gly	ttg Leu 295	aca Thr	aca Thr	gct Ala	tgt Cys	att Ile 300	gtg Val	aat Asn	ata Ile	gga Gly	912
gcc Ala 305	cag Gln	aca Thr	agt Ser	aca Thr	gta Val 310	gtt Val	tgt Cys	gtc Val	gag Glu	gat Asp 315	ggg Gly	gtc Val	tca Ser	ttg Leu	cca Pro 320	960
aat Asn	act Thr	gaa Glu	aag Lys	att Ile 325	tta Leu	cct Pro	ttt Phe	gga Gly	gga Gly 330	gag Glu	gat Asp	ata Ile	tgt Cys	aga Arg 335	tgc Cys	1008
ctt Leu	cta Leu	tgg Trp	att Ile 340	cag Gln	agg Arg	cat His	tac Tyr	caa Gln 345	aag Lys	tgg Trp	cca Pro	caa Gln	atc Ile 350	aac Asn	aca Thr	1056
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gag Glu	tca Ser 370	ttt Phe	tgt Cys	gaa Glu	att Ile	aga Arg 375	gca Ala	gga Gly	gaa Glu	ctt Leu	gaa Glu 380	act Thr	gtt Val	gca Ala	acg Thr	1152
gtt Val 385	cat His	tct Ser	tat Tyr	gag Glu	gaa Glu 390	ggc Gly	atg Met	cca Pro	gct Ala	gtg Val 395	cct Pro	cac His	aag Lys	aca Thr	aat Asn 400	1200
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tac Tyr	gag Glu	aat Asn 435	atg Met	ttg Leu	gaa Glu	gac Asp	act Thr 440	tgg Trp	aac Asn	atg Met	gac Asp	ttt Phe 445	gga Gly	ggt Gly	ggt Gly	1344
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 Asp Thr Val Gln Val Leu Pro Ser Arg Thr Glu Pro Gln Phe Val Thr
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 Trp Ile Glu Arg His Gln Trp Met Val Asn Gly Val Asn Lys Gly Gly
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 Gln Ser Gly Lys Pro Thr Val Val Asp Gln Met Leu Asn Thr Glu Val
 65 70 75 80
 Thr Thr Asn Gln His Val Asp Arg Glu Arg Ala Tyr Asn Ser Ala Ala
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Ser Leu Leu Lys Ile Leu Phe Leu Asp Glu Ser Ser Ser Ser Gly Ser
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 Ser Glu Ser Lys Arg Lys Tyr Arg Lys Met Ile Phe Gly Glu Glu Ala
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 Arg Gly His Phe Asn Val Ser Pro His Tyr Ser Ala Gln Arg Val Cys
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 Ile Thr His Lys Glu Arg Phe Ser Phe His Ala Val Ile Val Val Pro
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 Ala Val Phe Gly Asn Gly Leu Thr Thr Ala Cys Ile Val Asn Ile Gly
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Glu Ser Phe Cys Glu Ile Arg Ala Gly Glu Leu Glu Thr Val Ala Thr
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Val His Ser Tyr Glu Glu Gly Met Pro Ala Val Pro His Lys Thr Asn
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Lys Pro Lys Lys Glu Glu Lys Ile Gly Leu Ala Glu Ala Ile Thr Ser
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Ser Ile Gln Leu Ile Gly Gly Ala Gly Leu Thr Lys Gly Leu Val Ala
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Ala Val Glu Glu Arg Val Leu His Ala Ile Pro Pro Thr Glu Ala Ile
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Asp Thr Val Gln Val Leu Pro Ser Arg Thr Glu Pro Gln Phe Val Thr
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